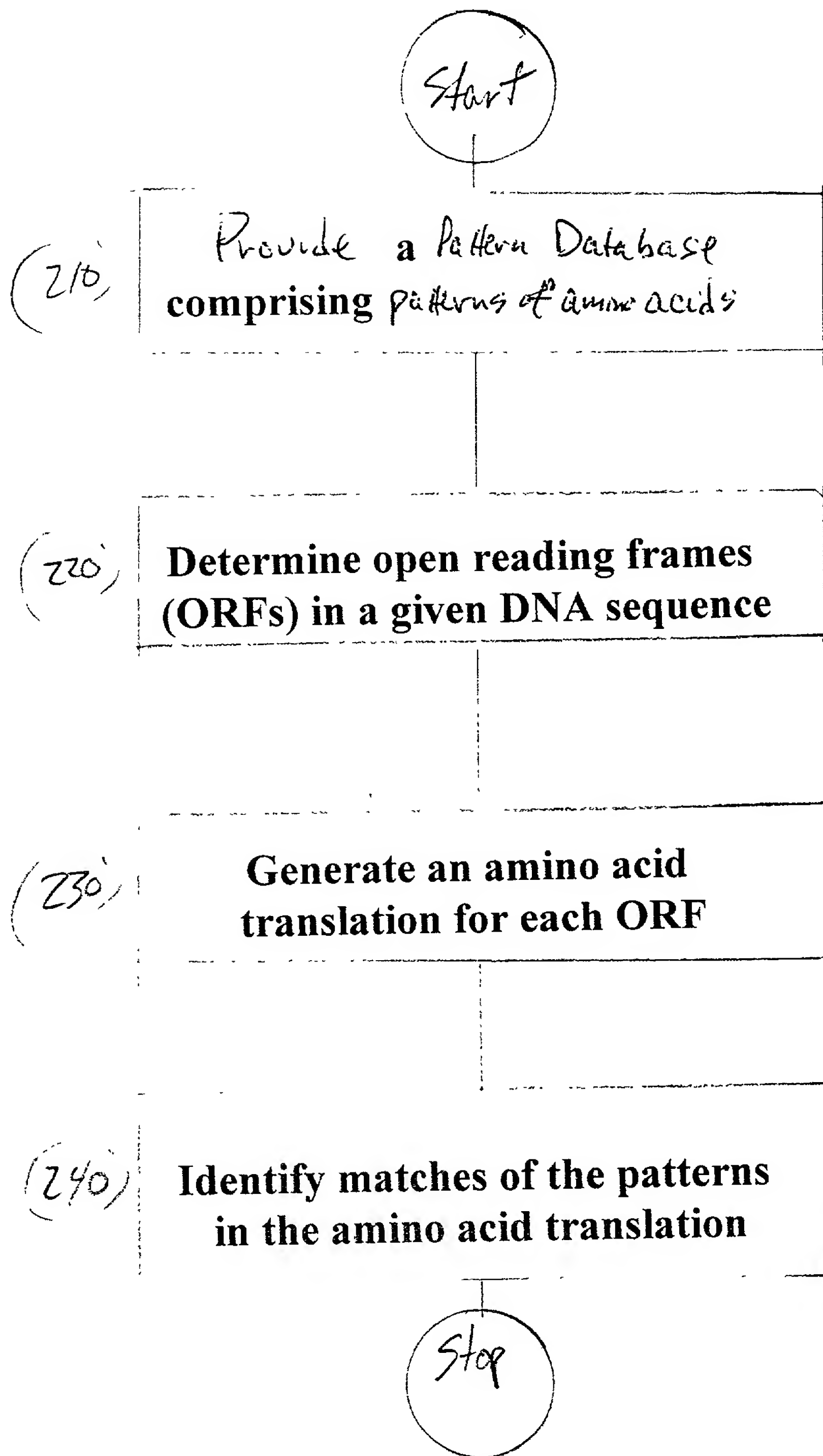


Figure 1



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Figure 2

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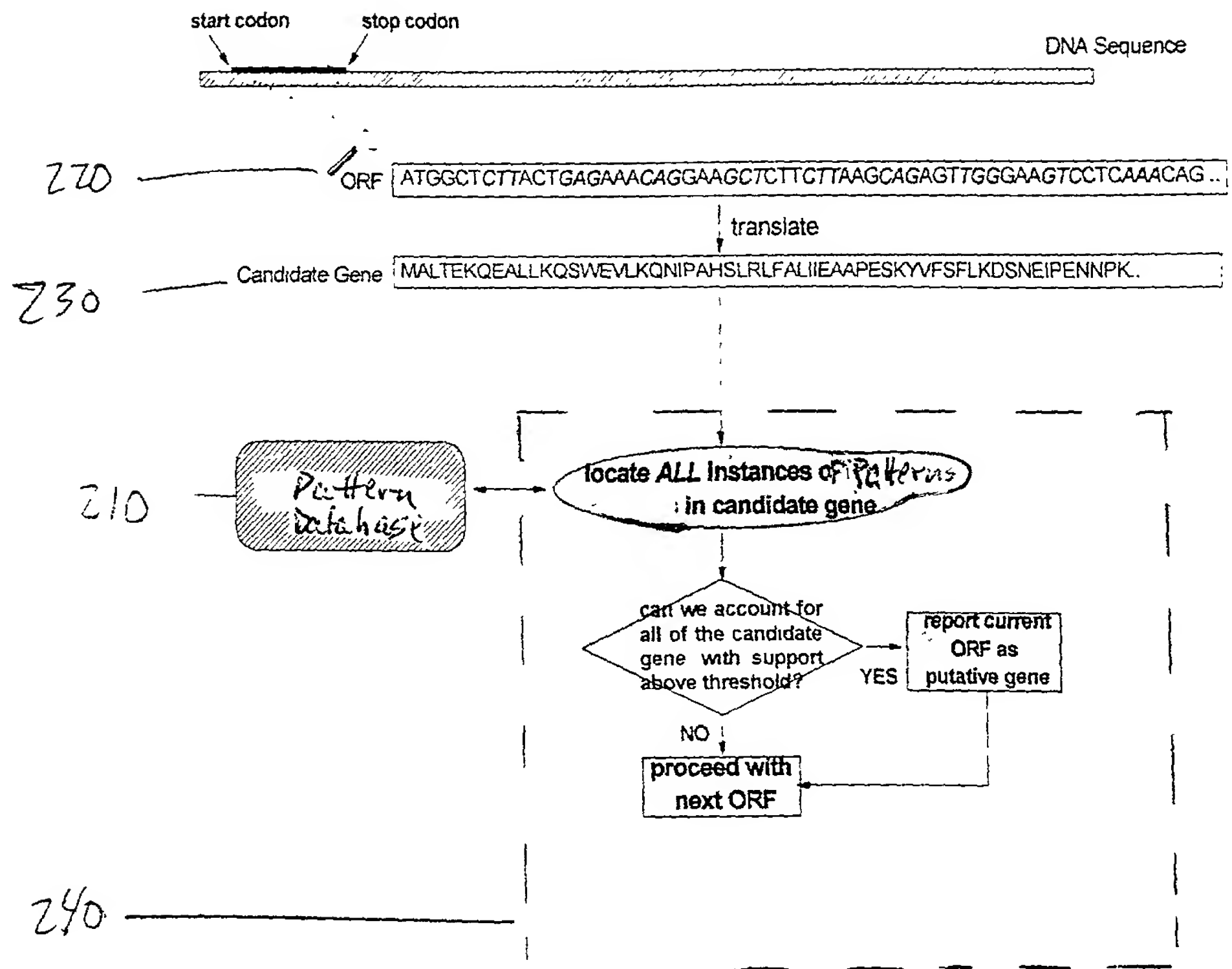


Figure 3

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#	Organism	Abbr.	Length	#ORF	#CDS
1	Archaeoglobus fulgidus DSM4304	AF	2,178,400	73,238	2,407
2	Methanococcus jannaschii DSM2661	MJ	1,664,970	74,456	1,715
3	Methanobacterium thermoautotrophicum delta H	MT	1,751,377	64,726	1,869
4	Pyrococcus abyssi GE5	PA	1,765,118	64,436	1,765
5	Aquifex aeolicus VF5	AA	1,551,335	50,591	1,523
6	Borrelia burgdorferi B31	BB	910,724	40,403	850
7	Bacillus subtilis 168	BS	4,214,814	167,735	4,101
8	Campylobacter jejuni NCTC11168	CJ	1,641,481	72,016	1,635
9	Chlamydia pneumoniae CWL029	CPc	1,230,230	50,872	1,052
10	Chlamydia pneumoniae AR39	CPa	1,229,853	50,840	1,110
11	Chlamydia trachomatis serovar D	CT	1,042,519	42,338	894
12	Escherichia coli K12-MG1655	EC	4,639,221	163,600	4,285
13	Haemophilus influenzae KW20	HI	1,830,138	83,944	1,709
14	Helicobacter pylori 26695	HP	1,667,867	67,227	1,567
15	Rickettsia prowazekii Madrid E	RP	1,111,523	53,656	835
16	Synechocystis sp. PCC6803	SS	3,573,470	141,204	3,182
17	Thermotoga maritima MSB8	TM	1,860,725	57,584	1,846

Table / Details on the 17 genomes used in our experiments.

Figure 4(a)

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	(a) 1.0 x #CDS					(b) 1.1 x #CDS				
	Annotated	Add itional	Hits	Score		Annotated	Add itional	Hits	Score	
AF	2319	96.3	88	41	272.0	2381	98.9	267	55	103.7
MJ	1689	98.5	26	7	148.6	1715	100.0	172	12	18.0
MT	1816	97.2	53	6	166.2	1853	99.1	203	9	79.2
PA	1742	98.7	23	5	188.7	1765	100.0	177	20	9.7
AA	1491	97.9	32	6	418.3	1520	99.8	156	25	69.2
BB	850	100.0	0	0	18.0	850	100.0	86	0	0.8
BS	3959	96.5	143	15	214.9	4043	98.6	470	39	108.0
CJ	1630	99.7	5	0	9.2	1634	99.9	165	0	0.7
CPc	1050	99.8	2	1	48.5	1052	100.0	106	5	2.3
CPa	1104	99.5	6	3	13.1	1110	100.0	111	5	2.1
CT	892	99.8	2	2	56.4	893	99.9	91	2	2.4
EC	3958	92.4	327	24	595.1	4062	94.8	652	35	418.4
HI	1697	99.3	12	6	78.8	1709	100.0	171	31	10.1
HP	1552	99.0	15	10	33.7	1565	99.9	159	15	1.5
RP	833	99.9	1	1	76.6	834	100.0	84	2	1.7
SS	3001	94.5	174	4	408.4	3068	96.6	425	8	267.1
TM	1781	96.5	65	27	336.6	1813	98.2	218	37	159.6

Table Z. Prediction with optimal seqlet weights for each genome.

Figure 4(b)

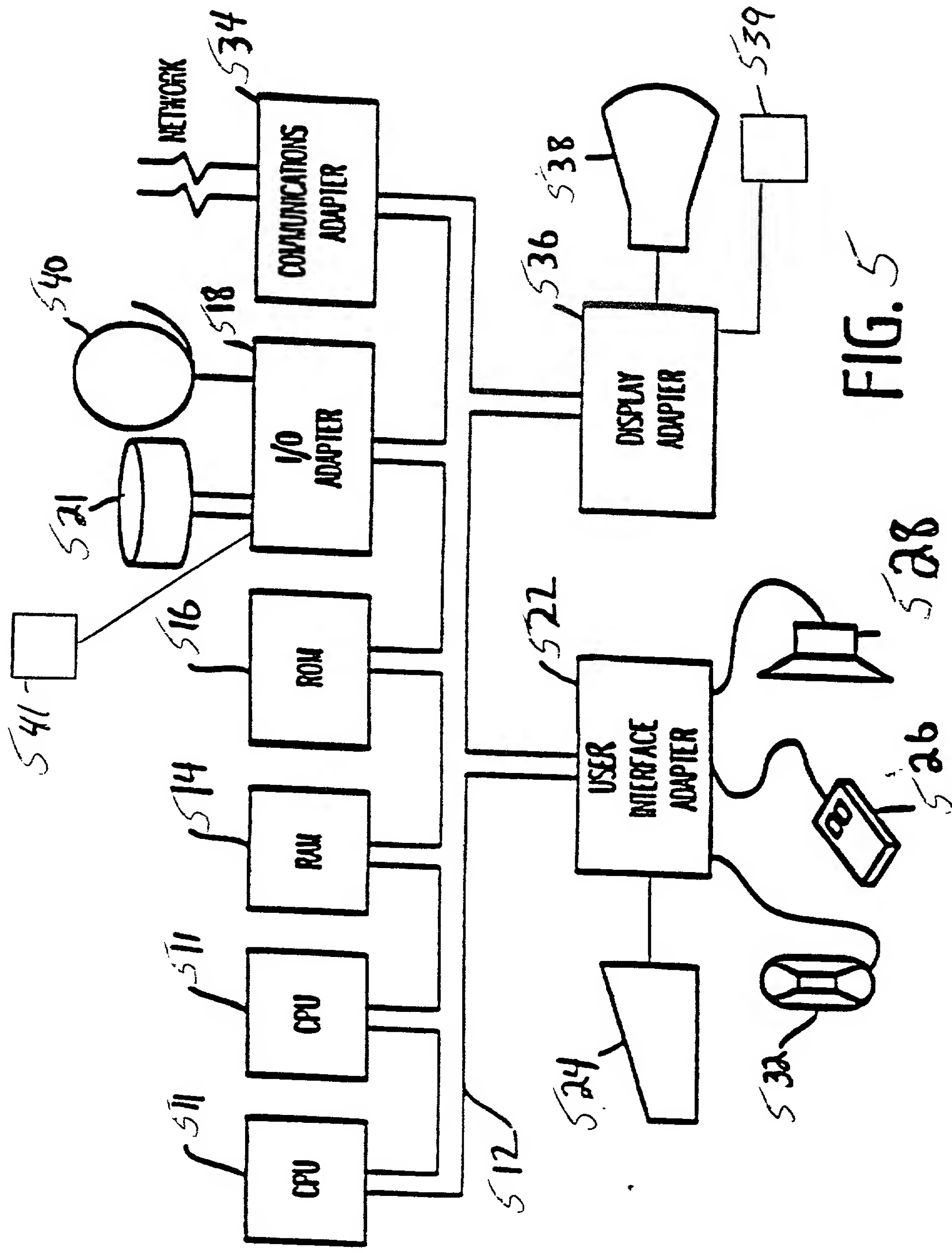


FIG. 5

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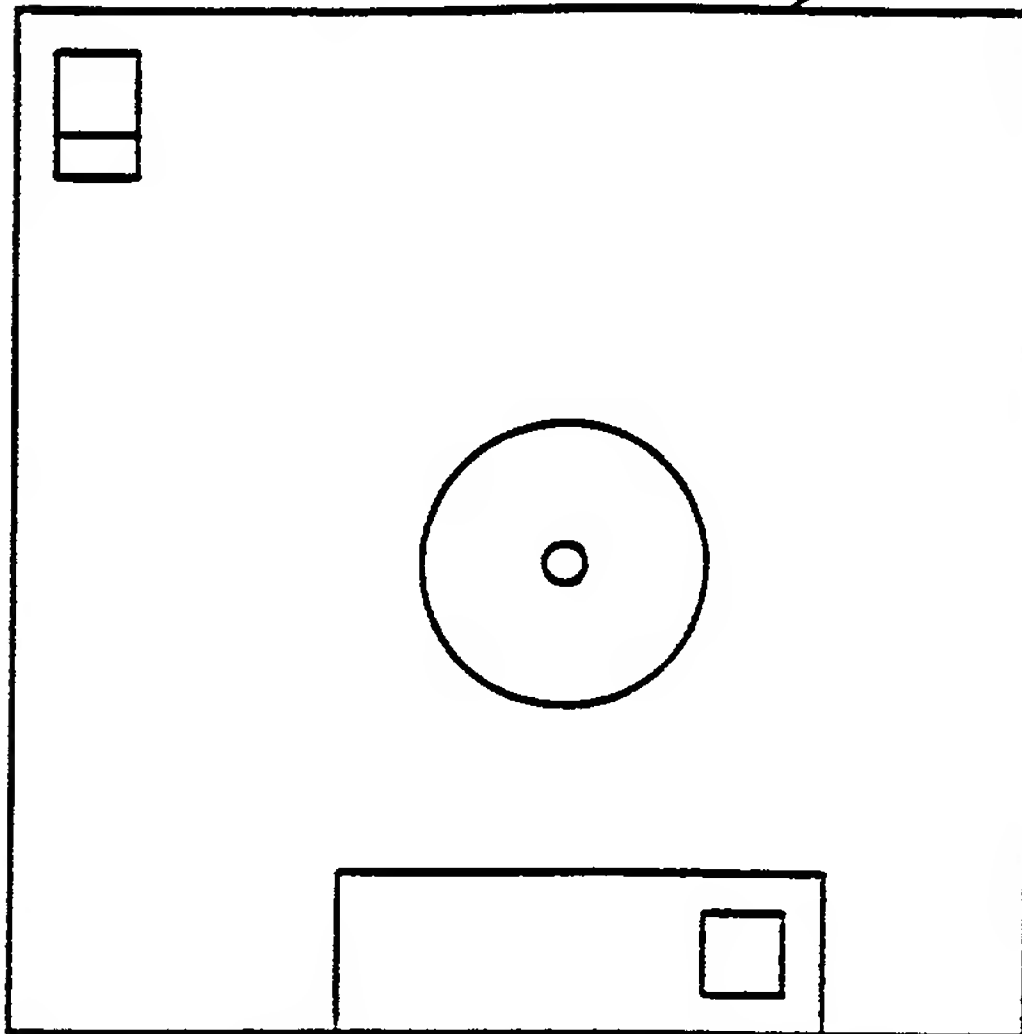


FIGURE 6

1005344.013100